

Result No.	Score	Query Match	Length	DB	ID	Description
1	203.4	8.1	936	22	AAF58252	oligonucleotide D1
2	203.4	8.1	936	22	AAF58254	oligonucleotide D1
3	203.4	8.1	936	22	AAF58257	oligonucleotide D1
4	203.4	8.1	936	22	AAF58259	oligonucleotide D1
5	203.4	8.1	936	22	AAF58262	oligonucleotide D2
6	203.4	8.1	938	22	AAF58255	oligonucleotide D1
7	195.4	7.8	936	22	AAF58252	oligonucleotide D1
8	195.4	7.8	936	22	AAF58254	oligonucleotide D1
9	195.4	7.8	936	22	AAF58257	oligonucleotide D1
10	195.4	7.8	936	22	AAF58259	oligonucleotide D1
11	195.4	7.8	936	22	AAF58262	oligonucleotide D2

C	12	195.4	7.8	238	22	AAFS58255	Oligonucleotide D1
C	13	68.2	2.7	944	22	AAFS62338	Oligonucleotide D1
C	14	67.6	2.7	244	22	AAFS62338	Oligonucleotide D1
C	15	58.4	2.3	664	20	AAHX3181	Base sequence of t
C	16	58.4	2.3	732	20	AAHX3181	Base sequence of t
C	17	58.4	2.3	797	20	AAAX3180	Complex virus bar f
C	18	58.4	2.3	7996	20	AAAX3180	Base sequence of t
C	19	56.2	2.2	2418	13	AAO27886	P. falciparum GBPI3
C	20	56	2.2	19124	18	AAAT72882	Plasmodium var-7 g
C	21	56	2.2	19124	21	AAZ96287	Plasmodium var-7 g
C	22	51.4	2.1	605	17	AAZ31530	Human 3' apolipoprotein
C	23	49.8	2.0	665	21	AAZ31996	Human apolipoprotein
C	24	48.8	2.0	19124	18	AAAT72882	Plasmodium var-7 g
C	25	48.8	2.0	19124	21	AAZ96287	Plasmodium var-7 g
C	26	48.6	1.9	549	21	AAAG94393	Cat flea head and
C	27	48.6	1.9	549	21	AAAG94393	Cat flea head and
C	28	47.8	1.9	3101	11	AAAO02047	Sequence encoding
C	29	47.6	1.9	20674	21	AAAC58012	Arachidonic acid m
C	30	47.6	1.9	1052	10	AAAC90224	Malaria-specific t
C	31	47.2	1.9	8920	15	AAAG62924	Carbamoyl-phosphat
C	32	46.8	1.9	1212	21	AAAT02018	Plasmodium falcipar
C	33	46.8	1.9	1711	19	AAV33136	Plasmodium berghei
C	34	46.8	1.9	4350	7	AAAG60472	Sequence encoding
C	35	46.8	1.9	9048	18	AAAT43225	Brassicica napus FC2
C	36	46.4	1.9	5059	20	AAAX84332	Sealth virus nucle
C	37	46.2	1.8	2040	21	AAAT70158	Plasmodium falcipar
C	38	46.2	1.8	5760	6	AAAS0530	Sequence encoding
C	39	46	1.8	6621	21	AAAT70188	Plasmodium falcipar
C	40	45.8	1.8	11011	21	AAAC68252	B. burgdorferi toxin
C	41	45.8	1.8	910715	20	AAAX20248	Borrelia burgdorferi
C	42	45.4	1.8	5852	12	AAAT17110	Dicystostellium plas
C	43	45	1.8	977	21	AAZ626706	Candida albicans f
C	44	45	1.8	1034	21	AAZ52527	Human secreted prote
C	45	45	1.8	3101	11	AAAO02047	Sequence encoding

ALIGNMENTS

XX	RESULT	1
XX	ID	AAF58252 standard; DNA; 936 BP.
XX	AC	AAF58252.
XX	DT	24-APR-2001 (first entry)
XX	DE	Oligonucleotide D1835.
XX	KX	Electron-transfer group; ETM; mismatch; genotyping;
XX	KW	gene expression; ss.
XX	OS	Synthetic.
XX	PN	WO200107665-A2.
XX	PD	01-FEB-2001.
XX	PF	26-JUL-2000; 2000MO-US20476.
XX	PR	26-JUL-1999; 99US-0145695.
XX	PR	17-MAR-2000; 2000US-0190259.
XX	PA	(CLIN-) CLINICAL MICRO SENSORS INC.
XX	PI	Umek RM;
XX	DR	WPI; 2001-159728/16.
XX	PT	Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
XX	XX	

PS Example 6; Page 127; 159pp; English.

XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.

XX Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 8.1%; Score 203.4; DB 22; Length 936;
Best Local Similarity 3.9%; Pred. NO. 6.3e-29;
Matches 33; Conservative 551; Mismatches 267; Indels 0; Gaps 0;

QY 1504 tactgaacactggtgttcgatactgctatattgctataataaacaacgtcaatt 1563
DB 1 www.
QY 1564 atatacgaatttttcggaatttaacgcatactgtaagataataacatgcatg 1623
DB 61 www.
QY 1624 gtttcaaatcatatgatgaacgacgacgaagtgctactactcctcaaatatgcat 1683
DB 121 www.
QY 1684 gagagagatatgtattataaatttatttttgaagaagaataagagggaagttactg 1743
DB 181 www.
QY 1744 ggtgagtcgatgtaaaacaaagaagaagaacgaacccataacgcatcatgata 1803
DB 241 www.
QY 1804 tcgacctctatccttctccttcttatttcttcgaagacttttctactaat 1863
DB 301 www.
QY 1864 gaacactccaactatctaactatacaactcgcattgataaagaatatataaga 1923
DB 361 www.
QY 1924 tactgtgatatttttaactagaataatattgctctgtaattttcgttaagtaaat 1983
DB 421 www.
QY 1984 caacattttcagtagaacaataatctacgcaaaagtagatcatttltgtccaa 2043
DB 481 www.
QY 2044 aatctcagtagtataggtgtgtagtaaaaaaacaacattctgattgcccacaa 2103
DB 541 www.
QY 2104 aataaagagagaagaataatgttcaaaagtgctctctctcctaattgttttc 2163
DB 601 www.
QY 2164 actaaaccgaatagatccaacagctctacaagtcocaaagaataacatggagacaa 2223
DB 661 www.
QY 2224 ttgatgcaaaaatactccttctcatgctctttttatctctagcttttaattact 2283
DB 721 www.
QY 2284 aataaactcacaaatccacaaacccattctctacaactcacctcatgatttac 2343
DB 781 www.
QY 2344 cgaactccacac 2354

DB 841 cccccccccc 851

RESULT 2

AAFS8254

ID AAF58254 standard; DNA; 936 BP.

AAFS8254;

24-APR-2001 (first entry)

oligonucleotide D1875.

Electron-transfer group; ETM; mismatch; genotyping;

gene expression; ss.

Synthetic.

WO200107665-A2.

01-FEB-2001.

26-JUL-2000; 2000MO-US20476.

26-JUL-1999; 9905-0145695.

17-MAR-2000; 2000US-0190259.

(CLIN-) CLINICAL MICRO SENSORS INC.

umek RM;

WPI; 2001-159728/16.

Nucleic acids containing electron-transfer group, useful as labels in

hybridization assays, e.g. for genotyping, allowing repeat analyses on

a single surface

Example 6; Page 127; 159pp; English.

The present invention relates to a composition comprising two nucleic

acids each containing an electron-transfer group (ETM) having

different redox potentials. The invention is used for electronic

detection of nucleic acids, especially of substitutions (mismatches)

and single-nucleotide polymorphisms, e.g. for genotyping,

monitoring gene expression.

Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

Query Match 8.1%; Score 203.4; DB 22; Length 936;

Best Local Similarity 3.9%; Pred. NO. 6.3e-29;

Matches 33; Conservative 551; Mismatches 267; Indels 0; Gaps 0;

QY 1504 tactgaacactggtgttcgatactgctatattgctataataaacaacgtcaatt 1563
DB 1 www.
QY 1564 atatacgaatttttcggaattttacgcatactgtaagataataacatgcatg 1623
DB 61 www.
QY 1624 gtttcaaatcatatgatgaacgacgacgaagtgctactactcctcaaatatgcat 1683
DB 121 www.
QY 1684 gagagagatatgtattataaatttatttttgaagaagaataagagggaagttactg 1743
DB 181 www.
QY 1744 ggtgagtcgatgtaaaacaaagaagaagaacgaacccataacgcatcatgata 1803
DB 241 www.

```
OY 1804 tcgaccttctatcttctcctcttatttatttctcaggacttttctactaat 1863
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 360
OY 1864 gaaacctccaacttcttaactaactcctccatgtagaataaagaataataaga 1923
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 361 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 420
OY 1924 tatgtgatatttgttaactagaataatattgtctctgttaatttctgaagtaaat 1983
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 421 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 480
OY 1984 caacatttccagtagaacaataattactgcaaaagtagatcatatttctgcaa 2043
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 481 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 540
OY 2044 aatccagttagctataggtgttagtaaaaaaacaacatttgcctcccaaaa 2103
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 541 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 600
OY 2104 aataagagagaagaatatgttcaaaagtgtctctctctcctaattagtctc 2163
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 601 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 660
OY 2164 actaaacccaattagatcaaaacagctcaaaagtcacaaagataaacaatggagacaaa 2223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 661 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 720
OY 2224 ttcatgtcaaaaaaacctcttctcctcttcttcttctcctcagctcttcttaattact 2283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 721 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 780
OY 2284 aataaaactcaacaatacccaaacccattctctcaaacatccatctcatagattac 2343
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 781 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 840
OY 2344 ccaactccacac 2354
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 841 cccccccccc 851

RESULT 3
AF58257
ID AF58257 standard; DNA; 936 BP.
AC AF58257;
XX
XX 24-APR-2001 (first entry)
XX
XX Oligonucleotide D1954.
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
XX gene expression; ss.
XX
XX Synthetic.
XX
XX MO200107665-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX Umek RM;
XX
XX WPI; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
```

```
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
PS
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
SQ

Query Match 8.1%; Score 203.4; DB 22; Length 936;
Best Local Similarity 3.9%; Pred. No. 6.3e-29;
Matches 33; Conservative 551; Mismatches 267; Indels 0; Gaps 0;

OY 1504 tactgaaacctgggtgttcatgtatttgcctcatataaacaacatcgttaatt 1563
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 60
OY 1564 atatacgaatttttctcgaaatttaacgcacatctgtaaglatataaacatgcatgctc 1623
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 120
OY 1624 gtttcaaatcatatgatgaacatccagtgtaagtgtctactactcctacaattgcat 1683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 180
OY 1684 gagaagatatgtatttaaatatttgaagaagaataagagggaagttaacttg 1743
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 240
OY 1744 ggtgcatcgtatgtaaaacaaagaagaagaagcgaacccaactaagcatatcatgata 1803
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 300
OY 1804 tcgaccttctatcttctcctcttatttatttctcagaacttttctactaat 1863
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 360
OY 1864 gaaacctccaactataactaactaactccatccatgtagaataaagaataatataaga 1923
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 361 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 420
OY 1924 tatgtgatatttgttaactagaataatattgtctctgtaatttctgtaagtaaat 1983
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DB 421 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 480
OY 1984 caacatttccagtagaacaataatattactgcaaaagtagatcatatttctgcaaa 2043
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DB 481 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 540
OY 2044 aatccagttagctataggtgttagtaaaaaaacaacatttgcctcccaaaa 2103
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 541 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 600
OY 2104 aataagagagaagaatatgttcaaaagtgctctctcctaatttctgcttctc 2163
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 601 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 660
OY 2164 actaaacccaattagatcaaaacagctcaaaagtcacaaagataaacaatggagacaaa 2223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 661 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 720
OY 2224 ttcatgtcaaaaaaacctcttctcctcttcttcttctcagctcttcttaattact 2283
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DB 721 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 780
OY 2284 aataaaactcaacaatacccaaacattctcaaacattcattcatagattac 2343
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```


DR WPI; 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface *

PS Example 6; Page 128; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.

SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match	Score	DB	Length
8.1%	203.4	22	936

Matches 33; Conservative 551; Mismatches 267; Indels 0; Gaps 0;

[illegible][illegible]

RESULT 6

ID AAF58255 standard; DNA; 938 BP.

AC AAF58255;

DT 24-APR-2001 (first entry)

DE 014gonucleotide D1876.

Electron-transfer group; ETM; mismatch; genotyping; KW

22 XX

XX
0000070700

2
1
1
1
2
2
2
1

XX	2000	200000	200000
XX	2000	200000	200000

XX	2	1000	0000	014000
XX	2	1000	0000	014000

PR 17-MAR-2000; 2000US-0190259

PA (CLIN-) CLINICAL MICRO SENSORS INC

PI Umek RM;

DR WPT; 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface *

PS Example 6; Page 127; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.

50 Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other,

Query Match	8.18; Score 203.4; DB 22; Length 938;
-------------	---------------------------------------

Matches 33; Conservative 551; Mismatches 267; Indels 0; Gaps 0;

```

OY 1504 tactgaacacccctgttggtcttcagatatttggccataataaacaacacccgtaatt 1563
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 60
OY 1564 atatacgaatttttctcggaattacgcacatctgtaagatatataacatgctgc 1623
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 120
OY 1624 gtttcaaatcatatagaagaaacgataccagtaagtgtctaactctcaaatltgcat 1683
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 180
OY 1684 gagagagatatgtattatataaatttaatttttgaagaagaataaagagggaagttaacttg 1743

```


[illegible]

	RESULT	13
ID	AAFS8238/C	
XX	AAFS8238 standard; DNA;	244 BP.
AC	AAFS8238;	
XX		
Df	24-APR-2001	(first entry)
DE	Oligonucleotide D1250:D1102.	
KW	Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.	
OS	Synthetic.	
PN	WO200107665-A2.	
PD	01-FEB-2001.	
PF	26-JUL-2000; 200OWO-US20476.	
PR	26-JUL-1999; 99US-0145695. 17-MAR-2000; 200OUS-0190259.	
PA	(CLIN-) CLINICAL MICRO SENSORS INC.	
PI	Umek RM;	
DR	WPt; 2001-159728/16.	
PT	Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping; allowing repeat analyses or a single surface -	
PS	Example 4; Page 120; 159pp; English.	
CC	The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) deletion of nucleic acids,	

Query Match	2.7%	Score 67.6;	DB 22;	Length 244;
Best Local Similarity	3.4%	Pred. No. 0.00046;		
Matches	7;	Conservative 150;	Mismatches 49;	Indels 0;
				Gaps 0;

b 2 ctacagwwwww..... 61
180. tatagcatatctaataatgtccgaactttcctactactagaanaatatgtagtta 233

[illegible]

D6 122 18
D7 300 ttatttatttttataatggtgcta 325

```
DB      182  www.....cgcta 207
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ID	AXX33181	standard; DNA; 6644 BP
XX		
AC	AXX33181;	

aa	
Df	25-JUN-1999 (first entry)
xx	
DE	Base sequence of the plasmid pRx-ires-bsr.

KM CompoX virus; bsr; viral vector; expression; apoptosis; resistance
 KM crna; bcl-2; bcl-x1; FLIP; survivin; IAP; adenovirus; cancer;
 KM autoimmune disease; graft rejection reaction; inflammation;

XX	Synthetic.
OS	
OS	Cowpox virus.
vv	

PN	WO9913073-A2
XX	
PD	18-MAR-1999.
XX	

PF	07-SEP-1998;	98WO-JP04010
XX		
PR	08-SEP-1997;	97JP-0259235
XX		

(MEMO) NEW GENCOAST ASIA PACIFIC INC
 PI Hamada H;
 XX

XX New apoptosis-resistant virus-sensitive cell

XX The present invention describes an apoptosis-resistant virus-sensitive
CC cell line into which an apoptosis resistance gene has been introduced.
CC

CC associated genes. These can then be used in a variety of diseases for
CC which the induction of apoptosis by gene transfer, or where the
CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
CC are useful as vectors for gene transfer which can be used to transfer

therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if adenovirus vector capable of

CC encountered one problem where if an adenovirus vector capable of
CC expressing an apoptosis-associated gene is introduced into animal cells,
CC the cells producing the virus will be destroyed because the period of
CC time required to induce cell death by apoptosis is shorter than that

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2001, 13:44:08 ; Search time 92.89 Seconds
(without alignments)
6100.204 Million cell updates/sec

Title: US-09-578-827A-4

Sequence: 1 agaacgagcgcgtg99gtt.....ttcataaaaaaaaaaatg 2502

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 segs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents-NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Backfilestl.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	96.2	3.8	7218	1	US-08-232-463-14 Sequence 14, Appl
C 2	56	2.2	19124	2	US-08-487-826B-13 Sequence 13, Appl
C 3	49.8	2.0	665	2	US-08-883-795A-36 Sequence 36, Appl
4	48.8	2.0	19124	2	US-08-487-826B-13 Sequence 13, Appl
5	47.2	1.9	7218	1	US-08-232-463-14 Sequence 14, Appl
6	47.2	1.9	8920	2	US-08-446-855A-1 Sequence 1, Appl
7	47.2	1.9	8920	4	US-09-150-741-1 Sequence 1, Appl
8	46.8	1.9	289	4	US-09-007-003-17 Sequence 17, Appl
9	46.8	1.9	289	4	US-09-244-796-17 Sequence 17, Appl
C 10	46.8	1.9	9048	3	US-08-973-273-4 Sequence 4, Appl
C 11	44	1.8	827	4	US-08-998-416-535 Sequence 535, App
C 12	43.6	1.7	782	2	US-08-998-416-224 Sequence 224, App
C 13	43.4	1.7	5655	3	US-08-996-685-1 Sequence 1, Appl
C 14	43.4	1.7	5655	3	US-08-996-685-1 Sequence 1, Appl
C 15	43.4	1.7	6243	2	US-09-056-075-1 Sequence 2, Appl
C 16	43.4	1.7	6243	2	US-09-056-075-1 Sequence 2, Appl
C 17	43.4	1.7	8457	1	US-08-107-755A-1 Sequence 1, Appl
C 18	43.4	1.7	8457	1	US-08-107-755A-1 Sequence 1, Appl
C 19	43.4	1.7	8457	1	US-08-544-332-1 Sequence 1, Appl
C 20	43.4	1.7	9919	3	US-08-880-179-1 Sequence 1, Appl
C 21	43.2	1.7	7244	4	US-08-378-313-26 Sequence 26, Appl
C 22	42.2	1.7	2454	4	US-09-419-459-1 Sequence 1, Appl
C 23	41.4	1.7	2454	4	US-08-359-696-3 Sequence 3, Appl
C 24	41.4	1.7	4507	2	US-08-568-459A-3 Sequence 3, Appl
C 25	41.4	1.7	4507	2	US-08-487-826B-3 Sequence 3, Appl
C 26	41.4	1.7	6060	5	PCT-US96-09430-7 Sequence 7, Appl
C 27	41.4	1.7	6152	4	US-08-973-462-1 Sequence 1, Appl

C 28	41.4	1.7	6768	1	US-08-107-755A-1 Sequence 1, Appl
C 29	41.4	1.7	8457	1	US-07-991-867B-1 Sequence 1, Appl
C 30	41.4	1.7	8457	2	US-08-544-332-1 Sequence 1, Appl
C 31	41.2	1.6	615	4	US-08-998-416-186 Sequence 186, App
C 32	41.2	1.6	773	4	US-08-998-416-385 Sequence 385, App
C 33	40.8	1.6	834	4	US-08-998-416-305 Sequence 305, App
C 34	40.8	1.6	5852	1	US-07-867-106-2 Sequence 595, App
C 35	40.6	1.6	660	4	US-08-998-416-595 Sequence 32, Appl
C 36	40.4	1.6	657	1	US-07-991-867B-32 Sequence 32, Appl
C 37	40.4	1.6	660	2	US-08-544-332-32 Sequence 32, Appl
C 38	40.4	1.6	660	2	US-07-991-867B-8 Sequence 8, Appl
C 39	40.4	1.6	1511	1	US-08-107-755A-8 Sequence 8, Appl
C 40	40.4	1.6	1511	2	US-08-544-332-8 Sequence 8, Appl
C 41	40.4	1.6	4810	3	US-08-852-629-11 Sequence 11, Appl
C 42	40.4	1.6	4838	3	US-08-852-629-15 Sequence 15, Appl
C 43	40.4	1.6	5361	4	US-08-973-462-2 Sequence 2, Appl
C 44	40.4	1.6	636	4	US-08-998-416-1137 Sequence 1137, Ap
C 45	40.2	1.6	636	4	US-08-998-416-1137

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: EP 91 114 300.6
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F15
US-08-232-463-14

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Query Match      3.8%; Score 96.2; DB 1; Length 7218;
Best Local Similarity 7.9%; Pred. No. 6,5e-12;
Matches 35; Conservative 254; Mismatches 152; Indels 0; Gaps 0;

QY 514 acatagtataatatgacacacacccccaaaagttgggaactctaataagtctagag 573
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1477 ACGTATCGATGCAAGTAGTTAAAGAGATAAGACATTGTGTACRRRRRRRRRRRRR 1418
QY 574 aataatagtcctcagtggtggagattcaagaagagacaatgaaggltatatagctta 633
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1417 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1358
QY 634 aacaaaaatgcgatcttagtggagaggtttaaatgaaacaagttagatgtaaga 693
Db 1337 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1298
QY 694 caagaaacaaagaagcatgcocctagatttcctagataataataacattgctgttat 753
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1297 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1238
QY 754 ataagtaaagaatgatgacacatttgttcttcttacggytaaatgtgaaagaaaaa 813
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1237 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1178
QY 814 atatgtaatttttgagaanaatctcaaatagtaagaaggtctatatgagaagaagaga 873
Db 1177 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1118
QY 874 aaagggaanaatagtcagagaatgagaaggttagagagcaaaaggaatgtgagc 933
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1117 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRA 1058
QY 934 ttgatgatgttgatgcagcg 954
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1057 TCCTCGACGTCGACGAAGC 1037

RESULT 2
US-08-487-826B-13/C
; Sequence 13, Application US/08487826B
; Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellemis, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERITHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH21.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550

```

```

TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match      2.2%; Score 56; DB 2; Length 19124;
Best Local Similarity   44.7%; Pred. No. 0.003;
Matches 304; Conservative    0; Mismatches 370; Indels    6; Gaps    2.

OY  1016 ttatatattttcttcacagcgtcttcttgtaactgataatgtagaccettaagtattta 1075
Db  16061 TTATGCGTATTATAATATATATATATATATATATATGTAGTAAGCTTGATCATTTGGGTATA 16002

OY  1076 tatcacgaatatacatccatagtaglcaacaanaatggcgaaaccttgcgaatttc 1135
Db  16001 TATATATATATATATGATGATATATATGTCAGTAGTAATTAATTTTTATTTTATTTTAA 15942

OY  1136 aaactcacttgtcacttgtagatgctaaggctttcacacagltttgaaaattagctgatct 1195
Db  15941 ATTAATTTTTTTTTATTTTTTTTTATTTTATTTCAATTAATTTTTTAAATTTTATTTAATTT 15882

OY  1136 gaaatcctttaatcagcatgttcttggtgcgaacgcttaacttcttgatttgatgc 1255
Db  15881 AAAATTTTTTATATATATATATTTTTTTTTATATTAATTAATTTTTTAAATTTATTTATTT 15822

OY  1256 aaaacttcagaagcgttcagaactccttacactaatcttcaaataatcgaattaagaaaa 1315
Db  15821 TTATTTAAATTAATTTTTTTTTTTTATTTATATGATATATATTTTTTTTTAACATTTTTTAATT 15762

OY  1316 aatagagtttccaigcaccag-tgittgatagiaacgtagtcgaggaaigtctaanaacgat 1374
Db  15761 TTTTTTATTTTATATGATATATATATTTTATTTTAATATATATTTTTTCTTTTTTTTGTTT 15702

OY  1375 catgagtttggtgttcatgattggttcagaactggttatagtagaacatcctaacttttcg 1434
Db  15701 TTATGATATATATTTTTTTTTTTTTTTTTTTTTTAAAGTTTTTTTTTTCCTGTTTGTATTTATTT 15642

OY  1435 ttagctcgttgattagaagtcgtaaagaagccttttatttaccacagcttgagacttgg 1494
Db  15641 TTTTATATCATTTTTTTTTTTTATATATAAAAATTTTTTTTTTATTTTTTTTGCATATACCTTTT 15582

OY  1495 gatcagatagtaacttgaacaacacttggttggttccaigtatattggtccataataaacaac 1554
Db  15581 CATTTTTTATTCOTATCAAATAATTTATATTTTATATTAATTTTATATATTTTAAAATAATTT 15522

OY  1555 atcgtaattatatacoggaatttttcoggaatttcaogccatactcgtgaagtataataac 1614
Db  15521 TTTCGCCATTTTTTTTTTTTTTTTTTTTTTAAATTT-----AATAAATTTTTTTTTTAATTC 15467

OY  1615 atgcatactgcgtttcaaaattcatagatgaacagatccagtaagtgctactactoctaca 1674
Db  15466 ATTTTTCTTTTTTTTCATTTTAAATTAATTTGTTTTATATTTCTTTTTTAAATTAATAATACA 15407

OY  1675 atatgcatgagagagatat 1694
Db  15406 TATATATTAATAATATATATAT 15387

RESULT 3
US-08-883-795A-36/c
Sequence 36, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor

```

TITLE OF INVENTION: Recombinant DNA Molecules and Expression
 FILE OF INVENTION: Vectors for Tissue Plasminogen Activator
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/883,795A
 FILING DATE: 27-JUN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gravelle, Micheline
 REGISTRATION NUMBER: 40,261
 REFERENCE/DOCKET NUMBER: 7841-062
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 665 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Rh 32
 US-08-883-795A-36

Query Match	2.0%;	Score 49.8;	DB 2;	Length 665;
Best Local Similarity	49.2%;	Pred. No. 0.028;		
Matches 160;	Conservative	0;	Mismatches 162;	Indels 3;
				Gaps 1

QY	995	taagaacattctctctcattttataataattacacatgctctcatgtaagtacaa	1054
Db	343	TATTAACATTTTAATTATTAATAATAGTATTAATAACATTTTAATTATTAATAAT	284
QY	1055	tggagacacttaagtattatataatcatgtaataatcttaaggtatcatatacaaatg	1114
Db	283	TATTAACATTTTAATTATTAATAATATTTATTAATAATAATTTTA---ATTATTAATAATTT	227
QY	1115	tcaagaacaatttgcgaattccaatcactactgctgaatcgtagatgctgaagcttccacagt	1174
Db	226	AATTAATAAATTTTAATTATTAATAAATATTTTAATTATAAATATTTAATAAATAATTT	167
QY	1175	tttgaacaattgctgtaagctgcgaattccttaattaagcaatgcttctgtgccaagctt	1234
Db	166	AATTATAAATTTTAATTATTAATAAATAATTTTAATTATAAATTTTAATAAATAATTT	107
QY	1235	aattcttgcattatgtaatgcacaaattccaagagcgttcgaactccttacactaatctt	1294
Db	106	AATTATAAATTTTAATTATTAATAAATAATTTTAATTATAAATAATTTTAATAATTTT	47
QY	1295	aaaaataatcgattacaagagaata	1319
Db	46	AATTATAAATAATTTTAATTATTAATAA	22

RESULT	4
US-08-487-826B-13	
: Sequence 13, Application US/08487826B	
: Patent No. 5993827	

GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelisen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

Query Match	2.0%	Score 48.8	DB 2	Length 19124
Best Local Similarity	43.3%	Pred. NO. 0.1		
Matches 405	Conservative 0	Mismatches 512	Indels 19	Gaps 3
QY 1564	atatacggatttttttcggaattttaaagccatctgtgaagtatatatacagcatgc	1623		
DB 15301	ATATATATATGCTATGATATATGATTTTCTGATATATGATTTTCTGGCTTAACGATATATA	15360		
QY 1624	gtttcaaatccatatgatgaaagcatccacgtaagtgctactactccctaacaattgcat	1683		
DB 15361	TATATGAGTATGCTGATGCTGATTTTATATATATATTTTATATATGATTTATATATA	15420		
QY 1684	ggagagagatgatttttaatttaatttttgaagaagaagaagaagggaaggttactcg	1743		
DB 15421	AAAAAATAATATAAAAACAAATTTATTTAAAAATGAAAAAAGAAAAATGAAATATAAAAA	15480		
QY 1744	ggtgatcgatgtgaaacaaagaagaagaagaacgaaacccataagccattacatgata	1803		
DB 15481	AATTTATTTAAAAATAAAAAAATAAAAAAAGAGAAAAATTTTTTAAAAAATATATA	15540		
QY 1804	tgcacccctctatcttttctcctcttatttatttctcgaagactttttctactaat	1863		
DB 15541	AAAAATTTATATTTAAATATATAAATTTTGATATGAAATAAAAAATGAAAAAGATTAACAATAA	15600		
QY 1864	gaacactccaaacttctaactaactaactccacatgtaagaataaagaagaattatataga	1923		
DB 15601	AATTTAAAAAATAATTTTATATATAAAAAATAATGATTTATAAAAAATAAAAAACAATAAGAA	15660		

```

1 NAME: BENT, Stephen A.
2 REGISTRATION NUMBER: 29,768
3 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (703)836-9300
6 TELEFAX: (703)683-4109
7
8 INFORMATION FOR SEQ ID NO: 14:
9
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 7218 base pairs
12 TYPE: nucleic acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
15
16 IMMEDIATE SOURCE:
17 CLONE: pT5pt-Fls
18
19 US-08-232-463-14
20
21 Query Match 1.98; Score 47.2; DB 1; Length 7218;
22 Best Local Similarity 5.6%; Pred. No. 0.18;
23 Matches 22; Conservative 206; Mismatches 164; Indels 0; Gaps 0;
24
25 Oy 993 ctctgatgatgttgatgacgcgcacgcttcttcacgcctgctccacactcacaca 992
26 Db 1086 yyytlyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1145
27 Oy 993 cctatgaacatctctctctatcttataatataatcacaatgctctatgta 1052
28 Db 1146 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1205
29 Oy 1053 aatgctgacacctaagatattatataatcattatatactatagatcacacaaat 1112
30 Db 1206 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1265
31 Oy 1113 gctctgaacacttctgcaattcactctactgtctcatgtgatgacgttccaat 1172
32 Db 1266 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1325
33 Oy 1173 gttctgaacatagctgacatcgaactcttaattagcatgttctgttgtaacgt 1232
34 Db 1326 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1385
35 Oy 1233 ttaattctgattatcagtcacaaaatccagagcgttcagaactctaacataatc 1292
36 Db 1386 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyygtaacaaattc 1445
37 Oy 1293 ttaaaataatcagatgaagagaaataagct 1324
38 Db 1446 tttatctcttttaactacttgcatgataagat 1477
39
40 RESULT 6
41 US-08-446-855A-1
42 Sequence 1, Application US/08446855A
43 Patent No. 5843573
44
45 GENERAL INFORMATION:
46 APPLICANT: Stewart, Thomas S
47 APPLICANT: Flores, Maria V
48 APPLICANT: O'Sullivan, William J
49 TITLE OF INVENTION: Nucleotide sequence encoding carbanoyl
50 NUMBER OF SEQUENCES: 2
51 CORRESPONDENCE ADDRESS:
52 ADDRESSEE: Nixon & Vanderhye PC
53 STREET: 1100 No. 5849573th Glade Road, 8th Floor
54 CITY: Arlington
55 STATE: Virginia
56 COUNTRY: USA
57 ZIP: 22201-4714
58
59 COMPUTER READABLE FORM:
60 MEDIUM TYPE: Floppy disk
61 COMPUTER: IBM PC compatible
62 OPERATING SYSTEM: PC-DOS/MS-DOS

```



```

1 SOFTWARE: PatentIn Release #1.24
2
3 CURRENT APPLICATION DATA:
4
5 APPLICATION NUMBER: US/08/446,855A
6
7 FILING DATE: 06-Jul-1995
8
9 CLASSIFICATION: 435
10
11 ATTORNEY/AGENT INFORMATION:
12
13 NAME: Mitchard, Leonard C
14 REGISTRATION NUMBER: 29,009
15
16 REFERENCE/DOCKET NUMBER: 47-80
17
18 TELECOMMUNICATION INFORMATION:
19
20 TELEPHONE: 703-816-4000
21
22 TELEFAX: 703-816-4100
23
24 INFORMATION FOR SEQ ID NO: 1:
25
26 SEQUENCE CHARACTERISTICS:
27
28 LENGTH: 8520 base pairs
29
30 TYPE: nucleic acid
31
32 STRANDEDNESS: single
33
34 TOPOLOGY: linear
35
36 MOLECULE TYPE: genomic
37
38 US-08-446-855A-1

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Query Match	1.9%	Score 47.2	DB 2	Length 8920
Best Local Similarity	44.5%	Pred. No.	0.19	
Matches 233; Conservative	0	Mismatches 288	Indels 3	Gaps 1

[illegible]

```

RESULT      7
US-09-150-741-1
: Sequence 1, Application US/09150741
: Patent No. 618396
: GENERAL INFORMATION:
:   APPLICANT: Stewart et al.
:   TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
:   Patent No. 618396
:   TITLE OF INVENTION: Synthetase II
:   FILE REFERENCE:

```

```

? CURRENT APPLICATION NUMBER: US/09/150,741
? CURRENT FILING DATE: 1998-09-10
? EARLIER APPLICATION NUMBER: PL6580
? EARLIER FILING DATE: 1992-12-16
? EARLIER APPLICATION NUMBER: AU93/00617
? EARLIER FILING DATE: 1993-12-02
? EARLIER APPLICATION NUMBER: 08/446,855
? EARLIER FILING DATE: 1995-07-06
? NUMBER OF SEQ ID NOS: 15
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1
? LENGTH: 8920
? TYPE: DNA
? ORGANISM: Plasmodium falciparum
US-09-150-741-1

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Query Match	1.98;	Score 47.2;	DB 4;	Length 8920;
Best Local Similarity	44.58;	Pred. No. 0.19;		
Matches 233;	Conservative 0;	Mismatches 288;	Indels 3;	Gaps 1;

[illegible]

RESULT 8
 US-09-007-005-17
 ; Sequence 17, Application US/09007005B
 ; Patent No. 6258538
 ; GENERAL INFORMATION:
 ; APPLICANT: Szostak, Jack W.
 ; APPLICANT: Roberts, Richard W.
 ; APPLICANT: Liu, Rihe
 ; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
 ; TITLE OF INVENTION: POSIONS
 ; FILE REFERENCE: 00786/350003
 ; CURRENT APPLICATION NUMBER: US/09/007,005B
 ; CURRENT FILING DATE: 1998-01-14
 ; EARLIER APPLICATION NUMBER: 60/035,963
 ; EARLIER FILING DATE: 1997-01-27

STREET: 1100 No. 6140085th Giebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,273
FILING DATE: 01-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCY/GB96/01332
FILING DATE: 03-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9511196.9
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MS Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9048 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear


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14
US-08-996-685-1/c
: Sequence 1, Application US/08996685
: Patent No. 6031153
:
: GENERAL INFORMATION:
:   APPLICANT: Ryals, John
:   APPLICANT: Friedrich, Leslie
:   APPLICANT: Uknes, Scott
:   APPLICANT: Molina, Antonio
:   APPLICANT: Russ, Wilhelm
:   APPLICANT: Knuff-Belter, Gertrude
:   APPLICANT: Kung, Ruth
:   APPLICANT: Kessmann, Helmut
:   APPLICANT: Oostendorp, Michael
:   TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
:   NUMBER OF SEQUENCES: 32
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: NO. 6031153artis Corporation
:     STREET: 3054 Cornwallis Road
:     CITY: Research Triangle Park
:     STATE: NO. 6031153ch Carolina
:     COUNTRY: US
:     ZIP: 27709
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/996,685
:     FILING DATE:
:       CLASSIFICATION:
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 08/761,543
:       FILING DATE: 6-DEC-1996
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 60/034,378
:       FILING DATE: 27-DEC-1996
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 60/034,379
:       FILING DATE: 27-DEC-1996
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 60/034,382
:       FILING DATE: 27-DEC-1996
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 60/034,730
:       FILING DATE: 10-JAN-1997
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 60/035,021
:       FILING DATE: 10-JAN-1997
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 60/035,022
:       FILING DATE: 10-JAN-1997
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 60/035,024
:       FILING DATE: 10-JAN-1997
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 08/875,015
:       FILING DATE: 16-JUL-1997
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Meigs, J. Timothy
:     REGISTRATION NUMBER: 38,241
:     REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGCI91153
:     TELEPHONE: (919) 541-8587
:     TELEFAX: (919) 541-8689
:   INFORMATION FOR SEQ ID NO: 1:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 5655 base pairs
:       TYPE: nucleic acid
:       STRANDEDNESS: single

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,179
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1909
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: exon
LOCATION: 2787..3347
OTHER INFORMATION: /product- "1st exon of NIM1"
FEATURE:
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LOCATION: 3427..4162
OTHER INFORMATION: /product- "2nd exon of NIM1"
FEATURE:
NAME/KEY: exon
LOCATION: 4271..4474
OTHER INFORMATION: /product- "3rd exon of NIM1"
FEATURE:
NAME/KEY: exon
LOCATION: 4586..4866
OTHER INFORMATION: /product- "4th exon of NIM1"
FEATURE:
NAME/KEY: CDS
LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
US-08-880-179-2

Query Match      1.7%; Score 43.4; DB 3; Length 5655;
Best Local Similarity 49.3%; Pred. No. 1.1;
Matches 113; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1769 agaaaaagcgaacccttaagcattacatgatacgcacctcttcttccctt 1828
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1654 ATATTAAGTAAATAATATGCTTCGCGCTTTTACTTTGTTCTTAAATGAT 1595
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QY 1829 tatttatttctcaggaacttttctacttaatagaacctccaactactaact 1888
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DB 1594 AAGTTAAATAGTAAGTATTGATGATTTAAAGTAATTAACAATACTCTATAAC 1535
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QY 1889 acactcccatgtagaataaagaataataataagaatctgcatatttgtaactagaa 1948
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DB 1534 TCAATACGACATCATATTATTAATTTACTAATTAATCTTTGACAAATTTATGAAT 1475
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Search completed: November 22, 2001, 22:01:01
 Job time: 29813 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2001, 13:20:33 ; Search time 1858.82 Seconds
(without alignments)
12723.685 Million cell updates/sec

Title: US-09-578-827A-4

Perfect score: 2502
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1022815 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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DB 496 AA 437
QY 2052 ttacagtagggttgcagtaaaacacacacattcttattgcccc 2099
DB 436 TTTTWWAAATTAATTTTWTWTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 389

RESULT / 2

CNS005TE/c 997 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL060767.1 GI:4943573
VERSION AL060767.1 GI:4943573
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)

REFERENCE
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1.997
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR12K22"
/note="end : TET3"
BASE COUNT 89 a 99 c 13 g 258 t 538 others
ORIGIN

Query Match

Best Local Similarity 19.6%; Pred. No. 1.1e-06;
Matches 119; Conservative 180; Mismatches 307; Indels 0; Gaps 0;

QY 482 aattagaggttcacataacataacagtagacatattgataataatgaacacacac 541
DB 917 RARARAGRGAGGCGGCGGRRRAAARARARARARARARARARARARARARARAR 858
QY 542 caaaaagtggaatcatataatagtagtagaataatagtcctcagggagagatca 601
DB 857 RRRRRGAGRRRRAGAGRRGRRGRRRRARARARARARARARARARARARARARR 798
QY 602 aagagagacatagaggtatataagactaaacaaatggcatgactgagagag 661
DB 797 RAGRRRRRANGARRRRRRGRRGRRRRRRARARARARARARARARARARARRA 738
QY 662 ggtttaaattgaacaagtagagttgaagaacagaacaaagagagcatgcctagat 721

DB 737 GAARRRARRRRRRRRGAGARRRRARRARARAGAAARRRRRGAGARRRRRG 678
QY 722 ttctgagtaaatatcacatctgctgttataaggaagagatatgacactgt 781
DB 677 RGRRRGAGRRRRRRRRMTTRARRRRRRRRRAGAAARRARRRRRRRRRRRRR 618
QY 782 tggttcttcacggtcaatctgaagaaaaaaatagtaataattgagaaaaat 841
DB 617 GRRRRAGRRRRRRRARRARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 558
QY 842 agtaagaggtatataatgagagaagagaagaaaggaataatgagagagag 901
DB 557 RRRARRRRRRRRRRARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 498
QY 902 gagaggttagagggcaaggaatgagagcttgatgatgattgtagacgcctcagc 961
DB 497 RRAAGARRRRRAAARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 438
QY 962 ttcttcacgctctcctcactcacacactatgacatctctctctataaa 1021
DB 437 NT 378
QY 1022 ttataatcacatgctctctgtaactatgtaagtgtagcacactaagtattatc 1081
DB 377 TTTTNT 318
QY 1082 atgtaat 1087
DB 317 TTATAT 312

RESULT 3

CNS003BD 1101 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR08K08 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL064091.1 GI:4941847
VERSION AL064091.1 GI:4941847
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

REFERENCE
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1.1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR08K08"
/note="end : TET3"

BASE COUNT	395 a	120 c	103 g	334 t	149 others
ORIGIN					

Query Match	3.4%	Score 84.2;	DB 219;	Length 1101;
Best Local Similarity	38.5%;	Pred. No. 4.4e-06;		
Matches 235;	Conservative 70;	Mismatches 301;	Indels 5;	Gaps 1

QY 1639 Tgataacagatccaaagttaagtgctactcactcctaacttgcattgtcatgaaggagtagtat 1698
Db 440 TTAAATHAACACTHCCAAAACCCTTYTTCCKCMKCMAMMMMAAAAAAAAAAATTTA 499
QY 1659 ttacaatttcattttgagaagaataagagggaaggttacctgggtgatcgatgta 1758
Db 500 AAAAAWMAAACCTTAATTATAAWMAAAAAWAAMAATAAATAAATTTTWTWMAMTTAA 559
QY 1759 aaacaaaagaagaagaacgaaaccacacgaacatltacatgcgcccttctatct 1818
Db 560 TAAATNAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTTTTTTTTTT 619
QY 1819 tttctccttatttattlcttctcaggacgttllcttactaatgaaaccaccaacta 1878
Db 620 TTTTTTTTAAWTTTWTATNTTTTAAATTTTAATTTTAATAATTTTATTAANNAAT 679
QY 1879 tctaactaacacacctcccaytagaataagaanaatlatalaagatatgttgtatlt 1938
Db 680 AAAAAAAAAAAAAAAAAAAAAAAAAATATATAAATAATTAATTAATTAATTAATWT 739
QY 1939 gtaactagaaaaatarattgtcgtcgttaatttttgtaagttaaacacattttca 1998
Db 740 AAANAATATATTAATAAA--AAATATWTTATTTATATTAATAATAWATWATTATA 794
QY 1999 gaacaaalatiactgcgaagaagtggatcataatttlgtccaacatccagtigcta 2058
Db 795 TATMNWATATWTTTWTAAATTATTAATWTAATWTAATWTAATTTTAATAATTA 854
QY 2059 taagggtcgttaaacaacaacacacctcgtgatttgcaccaaataaagagagaa 2118
Db 855 WAAAAAAAAATAATAAATAATATATWTAATWTAATWTAATWTAATAATWTAATAA 914
QY 2119 gaatatgtccaagaagtgctcctctcctcctcctaattatgatttcaactaacccaattg 2178
Db 915 AATTAATATAAAATTAATWATWTTTWTATTAATAAATWATWTAATAAATATTTTAT 974
QY 2179 atcaaacagctcacaaagtcacaaga laaacatlgggacgaacatctgcacaaatt 2238
Db 975 ATWATWATTTATTAATGWWMAAAAAAAAAAATAATWTAATAWMAAAYAAAWVACA 1034
QY 2239 cctctttcat 2249
Db 1035 AMTWATWAT 1045

RESULT 4

CNS00396 LOCUS CNS00396 GSS 03-JUN-1999

DEFINITION Drosophila melanogaster genome survey sequence TENG end of BAC #

BACR08K10 of RPECI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL063921 GI:4941778

VERSION AL063921.1 GI:4941778

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Preygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101) Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

COMMENT

The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library was prepared by Kazuhiro Oseguwa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial *NotI* digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y1; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Source

```

BASE COUNT      201 a      64 c      131 g      202 t      503 others
ORIGIN

```

Query Match	3.3%	Score 81.8	DB 219;	Length 1101;
Best Local Similarity	19.1%	Pred. No. 1.2e-05;		
Matches 125;	Conservative 291;	Mismatches 215;	Indels 22;	Gaps 2;

[illegible]

```

RESULT      5
CNS00EVL   1101 bp   DNA      GSS      04-JUN-1999
LOCUS      Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29B33 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069706
VERSION     AL069706.1 GI:4949849
KEYWORDS    GSS.
SOURCE      fruit fly.
            Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1101)
            Genoscope.
            Direct Submission
            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the library
            p1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
    source
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        /db_xref="taxon:7227"
        /clone_lib="RPCI-98"
        /clone="BACR29B33"
        /note="end : T7"
BASE COUNT   419 a      91 c      60 g      299 t      232 others
ORIGIN
Query Match      3.2%; Score 81.2; DB 219; Length 1101;
Best Local Similarity 36.7%; Pred. No. 1.6e-05;
Matches 217; Conservative 92; Mismatches 280; Indels 3; Gaps 2;
QY 1859 ttaatgaacctccaactctaactaactaactcactcactgtagaataaagaataata 1918
    ||||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 490 TWAATWAAAAAAMWMMWMTTWTWMMWMTTWTWMMWMTTWTWMMWMTTWTWMMWMTT 547
QY 1919 taagatcttgtagatcttgtagatcttgtagatcttgtagatcttgtagatcttgtag 1978
    ||||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 548 TAAATTTAAAMWMTATWMTTAAATTTAAAMWMTATWMTTAAATTTAAATTTAAATTTA 607
QY 1979 taatcaacattcttcagtagaacaataattactgcaaaaagtagagatcatctttctg 2038
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 608 TAAAAAAATATTTTWTATATAAATTTTAAATTAATTAATTAATTAATTAATTAATTTW 667
QY 2039 tccaaatccagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2098
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 668 WMTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 727
QY 2099 caaaaaataaagagagaagaataatgctcaaaagtgctctctctctctctctctctct 2158
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 728 AAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 787
QY 2159 ttctactaaaccatagatctcaaacagctcaaaagctcaaaagataaacaatagagac 2218

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DB 788 WATANAATATAAAMWMTATTAATTAATTAATAAAMWMTATTAATTAATAAAMWMTAT 847
QY 2219 aacatcgtatgcaaaaatcctcttcatgctcttcttcttcttcttcttcttcttctt 2278
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 848 AAAAAAATTAATTAATTAATTAATAAAMWMTATTAATTAATTAATTAATTAATAAAM 907
QY 2279 ttaataaataaatacacaatccacaacccattctctacacacccattctcttaga 2338
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 908 AATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 967
QY 2339 ttaccacccaccagagaacaagaataaataatatacatataataataaagaac 2398
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 968 TTWMTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1027
QY 2399 aacacatgagctg-atgaatatcacacaagaatataaactagat 2449
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 1028 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1079
RESULT      6
CNS00ITT   974 bp   DNA      GSS      03-JUN-1999
LOCUS      Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION BACR37D06 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL075432
VERSION     AL075432.1 GI:4954990
KEYWORDS    GSS.
SOURCE      fruit fly.
            Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 974)
            Genoscope.
            Direct Submission
            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            p1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
    source
        1..974
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        /db_xref="taxon:7227"
        /clone_lib="RPCI-98"
        /clone="BACR37D06"
        /note="end : TET3"
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ORIGIN
Query Match      3.1%; Score 77.6; DB 219; Length 974;
Best Local Similarity 33.9%; Pred. No. 7.6e-05;
Matches 285; Conservative 101; Mismatches 454; Indels 0; Gaps 0;
QY 1003 ttctctctatttataatattacacatgctctatgtaactatgtaaatgtagac 1062
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 65 TTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 124

```


[illegible]

	LOCUS	CNS00LT2	1101 bp	DNA	GSS	14-JUN-1999
	DEFINITION	Drosophila melanogaster genome survey sequence TERT3 end of BAC:				
		BACR4BP19 of RPCI-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.				
	ACCESSION	AL076714	GI:5102004			
	VERSION	AL076714.1	GI:5102004			
	KEYWORDS	GSS.				
	SOURCE	fruit fly.				
	ORGANISM	Drosophila melanogaster				
		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
		Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;				
		Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
	REFERENCE	1 (bases 1 to 1101)				
	AUTHORS	Genoscope.				
	TITLE	Direct Submission				
	JOURNAL	Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)				
	COMMENT	Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information please see http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw ap, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .				
	FEATURES	source 1..1101 /organism="Drosophila melanogaster"				
		/db_xref="taxon:7227"				
		/clone_lib="RPCI-98"				
		/clone-"BACR4BP19"				
		/note="end : TERT3"				
BASE COUNT		469 a	6 c	69 g	151 t	406 others
ORIGIN						
	Query Match	3.1%;	Score 76.6;	DB 219;	Length 1101;	
	Best Local Similarity	26.2%;	Pred. No. 0.00012;			
	Matches 269;	Conservative 212;	Mismatches 546;	Indels 0;	Gaps 0	
OY	510	gaagcattatgataaatgatgacacacacacacaaaagtgtggaaatcttaataatgtct	569			
Db	66	GAAGNNNNNNNAAANNAAANNNNNNACCAACCNNNEGBAANAANAANNNAAGAARAAGVGAAGG	125			
OY	570	agaagaataaagtcccttcagggttgaggatctcaagaagagagacaatgaaggtalatagac	629			
Db	126	AGRGAGADAAVAVTYRRAAAAAANNNNAAAANAANAANNNAANAANAANAANAANAANAANA	185			
OY	630	tctaaacaaaatgcacatgacttagtgggagaggttttaaatggaacaagtcgagtga	669			
Db	186	AAA	245			
OY	690	agaagaagaagaagaagaagcatgccctagattctcgagataaatlacacattctgtc	749			
Db	246	AAA	305			
OY	750	ctatatgaagtgagaagatacgacacattggttgttcttacggttaaatgtgaagaa	809			
Db	306	AAA	365			
OY	810	aaaaaatagtaattcttggaanaatcctaanaatgtaaagaggtatattggaagagaa	869			
Db	366	AAA	425			

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2001, 13:28:18 ; Search time 3308.22 Seconds

(Without alignments)
11698.227 Million cell updates/sec

Title: US-09-578-827A-4

Perfect score: 2502
Sequence: 1 agaaagcagcgcgtgggggtt.....ttcattaaaaaaaaaatg 2502

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_cm:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_pl1:*
- 13: gb_pl2:*
- 14: gb_pl3:*
- 15: gb_pl4:*
- 16: em_ba1:*
- 17: em_ba2:*
- 18: em_fun:*
- 19: em_htgo_hum:*
- 20: em_htgo_inv:*
- 21: em_htgo_rod:*
- 22: em_htg_hum1:*
- 23: em_htg_hum2:*
- 24: em_htg_hum3:*
- 25: em_htg_hum4:*
- 26: em_htg_hum5:*
- 27: em_htg_hum6:*
- 28: em_htg_hum7:*
- 29: em_htg_hum8:*
- 30: em_htg_inv1:*
- 31: em_htg_inv2:*
- 32: em_htg_inv3:*
- 33: em_htg_inv4:*
- 34: em_htg_rod:*
- 35: em_hum1:*
- 36: em_hum2:*
- 37: em_hum3:*
- 38: em_hum4:*
- 39: em_hum5:*
- 40: em_hum6:*
- 41: em_hum7:*
- 42: em_in:*
- 43: em_cm:*
- 44: em_or:*

- 44: em_ov:*
- 45: em_pat:*
- 46: em_ph:*
- 47: em_pl:*
- 48: em_rod:*
- 49: em_stg:*
- 50: em_sy:*
- 51: em_un:*
- 52: em_v1:*
- 53: gb_sts1:*
- 54: gb_sts2:*
- 55: gb_sts3:*
- 56: gb_sy:*
- 57: gb_un:*
- 58: gb_v11:*
- 59: gb_v12:*
- 60: gb_htg1:*
- 61: gb_htg2:*
- 62: gb_htg3:*
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- 89: gb_pr5:*
- 90: gb_pr6:*
- 91: gb_pr7:*
- 92: gb_pr8:*
- 93: gb_pr9:*
- 94: gb_rol:*
- 95: gb_rol2:*
- 96: gb_in4:*
- 97: gb_pr10:*
- 98: em_ba3:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2502	100.0	91740	13 ATFL9F18
2	2502	100.0	196339	13 ATCHRIV87
3	1201	48.0	2825	13 AF233752
4	96.2	3.8	7218	10 I66494
5	80.6	3.2	4601	6 DMU11584
6	80.6	3.2	19517	6 DMU37541
7	77	3.1	176174	86 AC007483
8	76.8	3.1	165097	84 CNS057CG

9	76.4	3.1	183250	62	AC012492	AC012492 Homo sapi
10	75	3.0	879	53	CNS01JRG	AL147405 Anopheles
11	72.8	2.9	176174	86	AC007483	AC007483 Homo sapi
12	71.8	2.9	5665	13	AF203688	AF203688 Canavalia
13	71.8	2.9	192929	60	AC005505	AC005505 Plasmidm
14	71.4	2.9	185800	81	AL512783	AL512783 Homo sapi
15	71.2	2.8	2305	96	S96842	S96842 SP96-spore-
16	71.2	2.8	7347	2	AF211124	AF211124 Carsonea1
17	71.2	2.8	148061	87	AC010727	AC010727 Homo sapi
18	70.2	2.8	94384	87	AC011718	AC011718 Homo sapi
19	69	2.8	183358	87	AC019041	AC019041 Homo sapi
20	68.8	2.7	68709	6	CER683B	AL032655 Caenorhab
21	68.8	2.7	110000	83	CE137H9_0	AL022597 Caenorhab
22	68.8	2.7	253516	83	CEYB3	AL022597 Caenorhab
23	68.8	2.7	330612	83	CEY7G2	AL022597 Caenorhab
24	68.4	2.7	160401	82	AC009277	AL033559 Plasmidm
25	68.2	2.7	253305	96	PFMAL3P7	AL355100 Homo sapi
26	67.8	2.7	184535	84	CNS05ETCJ	AL355100 Homo sapi
27	67.6	2.7	208546	76	AC083827	AC083827 Homo sapi
28	67.2	2.7	1141	10	AX083744	AX083744 Sequence
29	67.2	2.7	231912	77	AC087566	AC087566 Mus muscu
30	67	2.7	19517	6	DMU37541	U37541 Drosophila
31	67	2.7	165097	84	CNS05ETCG	AL355097 Homo sapi
32	66.6	2.7	964	54	CNS07EBR	AL441457 T7 end of
33	66.6	2.7	253305	96	PFMAL3P7	AL034559 Plasmidm
34	66.4	2.7	1141	10	AX083744	AX083744 Sequence
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36	66.2	2.6	156060	60	AC004153	AC004153 Plasmidm
37	66.2	2.6	174384	61	AC009524	AC009524 Homo sapi
38	65.8	2.6	4601	6	DMU11584	U11584 Drosophila
39	65.8	2.6	136098	86	AC006970	AC006970 Homo sapi
40	65.6	2.6	6372	6	DDICMPA	M23449 Dictyosellu
41	65.2	2.6	83440	68	AC024285	AC024285 Homo sapi
42	65.2	2.6	185603	74	AC073136	AC073136 Homo sapi
43	65	2.6	170157	79	AL355372	AL355372 Homo sapi
44	65	2.6	174565	74	AC069525	AC069525 Homo sapi
45	65	2.6	178087	85	AC005089	AC005089 Homo sapi

ALIGNMENTS

RESULT 1
ATF19F18 91740 bp DNA
LOCUS Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (RSSA project)
DEFINITION
ACCESSION AF035605
VERSION AF035605.1 GI:4468976
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE 1
AUTHORS Mewes, H.W., Mayer, K.F.X. and Schueller, C.
Unpublished
2 (bases 1 to 91740)
EU Arabidopsis sequencing project.
REFERENCE 2
AUTHORS Submitted (03-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schueller@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can be viewed at: <http://webserver.mips.biochem.mpg.de/Proj/thal/>.

COMMENT
FEATURES
Source 1. 91740

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5437. 5637
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5727. 5892

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QY	1801	atacgaaccttctatcttttccctcttatcttaattttcccgagactttcttcaact	1860
Dd	61521	atatgacaccttctatcttttccctcttatcttaattttcccgagactttcttcaact	61580
QY	1861	aatgaaacctccaacatctctaataaactcccatgtagaataaagaanaattata	1920
Dd	61581	aatgaaacctccaacatctctaataaactcccatgtagaataaagaanaattata	61640
QY	1921	agatatctgttatcttttgaactcgaagaatattttgctcgttaatttttcgtaagta	1980
Dd	61641	agatatctgttatcttttgaactcgaagaatattttgctcgttaatttttcgtaagta	61700
QY	1981	aatcaacatlttttcagtaagaacaaatatactgcgaagaagttagatcatatttttc	2040
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QY	2041	caaaatctcagcttagctataggttgctgtaglaaaaaacaacatcttgatttgc	2100
Dd	61761	caaaatctcagcttagctataggttgctgtaglaaaaaacaacatcttgatttgc	61820
QY	2101	aaaaataaagagagaaagaatattggtcagaagagtgctctctctctctaattagtt	2160
Dd	61821	aaaaataaagagagaaagaatattggtcagaagagtgctctctctctctaattagtt	61880
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Dd	61881	ttcactaaacccaacttagattccaacacgctctcaaaagtcgaagaataaactggagaa	61940
QY	2221	caattcgaatgcaaaaataatcctctcttcaatgctctttttatctctcgtgctttaa	2280
Dd	61941	caattcgaatgcaaaaataatcctctcttcaatgctctttttatctctcgtgctttaa	62000
QY	2281	actaaataaanaactcaaatccacaacaaacccatctctacaactcaactcatctga	2340
Dd	62001	actaaataaanaactcaaatccacaacaaacccatctctacaactcaactcatctga	62060
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Dd	62061	taccacatcccaacgagaaacacagaagaaaaatatacatatataataatacaagaa	62120
QY	2401	caacatgatctgtagtgaatatatacacaacaagatttaaatccttagatacttggtctcc	2460
Dd	62121	caacatgatctgtagtgaatatatacacaacaagatttaaatccttagatacttggtctcc	62180
QY	2461	ctttctcttatctatcttctctatctatctataaaaaaaaatg	2502
Dd	62181	ctttctcttatctatcttctctatctatctataaaaaaaaatg	62222

RESULT	2
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LOCUS	
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DEFINITION	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87.
ACCESSION	AL61591
VERSION	AL61591.2 GI:727073
KEYWORDS	
SOURCE	
ORGANISM	Thale cress. Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 42610 to 143618; 123423 to 196339) Rose,M., Hempel,S., Entlan,K.-D., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Unpublished 2 (bases 1 to 196339) EU Arabidopsis sequencing project. Direct Submission Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
REFERENCE	
AUTHORS	
JOURNAL	
TITLE	
JOURNALT	

QY	481	taattaaaggttcgcgatactaaataaacagcagacatctgataataatctaaacacaca	540
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ACCESSION AC007483
VERSION AC007483.7 GI:11991320
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 176174)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens, clone RP11-72A1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 176174)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckert, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
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Testaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.
DIRECT SUBMISSION
TITLE Submitted (05-MAY-1999) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 176174)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Boguslavsky, L., Bouhassira, B., Brown, A.,
Camarata, J., Campolano, A., Choepel, Y., Colangelo, M., Collins, S.,
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Jones, C., Karatas, A., Laroque, K., Lamazares, R., Landers, T.,
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Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zalnoun, J.,
Zemke, L., Zimmer, A. and Zody, M.
DIRECT SUBMISSION
TITLE Submitted (27-DEC-2000) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Dec 24, 2000 this sequence version replaced g1:11597092.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L642
Center clone name: 72_A_1

FEATURES
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location/Qualifiers
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repeat_region      45351. .45467  

                    /rpt_family="MIR"  

repeat_region      complement(45671. .45969)  

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repeat_region      complement(46397. .46526)  

                    /rpt_family="L2"  

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Best Local Similarity	42.9%;	Pred. No. 0.0023;		
Matches 819;	Conservative 0;	Mismatches 1070;	Indels 20;	Gaps 8;

Oy 544 aaagtggaagaaatcctaaataagtgtagagataataagccctaagtggaattccaa 603
 |||||
 Db 67596 AAAAATTTATATATATATTTACATATATATTTATATATATATATATATATATAT 676555
 Oy 604 gagagagcaatgaaggtatagatcctcaacaaaaatgcatgacttagtggagagg 663
 |||||
 Db 67656 TAATATATATTTATATATAAATACATGTTATATATATATATATATATATAAATACAT 67715
 Oy 664 tttaaattgaaacaagttagattgaagacaagaaaaaagaagcatgcccagattt 723
 GTATATATATATTTATATATATTTATATATATTTATATATATATATATATATATATAT 677555
 Db 67716 ctgagataataatlaacacttgctgttatataagtggaagaaatagacaacttgctg 783
 TTTATATATATATATATAAACAATTTTATATATATATATATATATATATAAATATCAT 678335

QY	784	glttccttaacgggaaactggaagaaataaaatgtaattcttggaagaacttaaaatag	843
Db	67836	AAATTAATAATTTTATGCTATTATATATATATATATTTTATATATATATTAATTAATTAATA	67895
QY	844	taaagaggtacatactggaagaagaagaagaagaagaatagtgcaagaatgga	903
Db	67896	TAAATATGATATATAT - ATATTAATAATATATATATATATATATATATATATATATATAT	67956
QY	904	gaggttcgagagaaagcgcaaatctggagcgcttgatgctgtgacgcgcgcgtt	963
Db	67955	TATATAGATATATATTTTATATATATTTTATATATATATATATATATATATATATATATAT	68014
QY	964	ttcttaacgcctctcccaactaacccacatgaacattccctctattataatt	1023
Db	68015	TTTATGATATAGATATATATTTTCTATATATATATATATATATTTCTATATATATATATAT	68074
QY	1024	atactcacatgctcactgcttaactgttaaatgctgaccacttaagattacatacat	1083
Db	68075	ATATTTCTATATATCATTTTAT	68130
QY	1084	gtatatactcttaaggtacatcacaaaatgctgacgaactttgcaattcaactact	1143
Db	68131	GTAATATATATTTT - TAT	68187
QY	1144	tgctcatctggaagtgtagcctttcaactgcttttgaaataatgctgactctgaattct	1203
Db	68188	AAATTTAATATTAATAATTTTAT	68247
QY	1204	ttaattgacatgctttctgttgccaagcttaattctctgtaactgtaactgccaatactc	1263
Db	68248	AAATTAATAATTTAT	68307
QY	1264	agagcgctcgaactctacactaaattctctaaaataatcgatlaagagaataagagt	1323
Db	68308	TTACATTAAT	68366
QY	1324	tttcacatgcacagtgctgtgtagtaacgtafcgcgcggaatgctctaaacgattagctt	1383
Db	68367	TAAATTAATAAT	68426
QY	1384	ggctttctgttgtagtagaactggcattagtagaactccaaacttttgtagcgtc	1443
Db	68427	GAT	68486
QY	1444	tgaattgaagatcgtaaaagagcctttattcttaaccaacgctggaactggatcgatag	1503
Db	68487	TTATATGAT	68546
QY	1504	tacttgaacaacttggctggcttctacgtattctggcctatatacaacaacacgtaatt	1563
Db	68547	TAAATATATCAAT	68603
QY	1564	attacagatctttctcgaatttaagcccatctgtaagtataatacatgacgtgc	1623
Db	68604	ATCAT	68663
QY	1624	gtttccaaattacatgataagacgaactccacgaagtgtactactccatacatgtgc	1683
Db	68664	TAT	68723
QY	1694	gagagagatatgattattataaatttaattcttgaaagaagaataaagagggaaggttactg	1743
Db	68724	AAATGAT	68783
QY	1744	ggggggtcgatggaaacaaagaagaagaagcgaaaccacacgaaccatcatgata	1803
Db	68784	AAATGTAATTAATAATTTTAT	68843
QY	1804	tgcgaactcttaactctttccctcttaattattcttcogaagccttttccacttaatt	1863
Db	68844	TAAAT	68902
QY	1864	gaaacctccaactactaactaatacaaccacatgtagaataagaataatatalaaga	1923

RESULT	9
AC012492	
LOCUS	AC012492 183250 bp DNA HTG 22-MAR-2001
DEFINITION	Homo sapiens chromosome YUK clone RP11-224B10, WORKING DRAFT
ACCESSION	AC012492
VERSION	AC012492.8 GI:13431121
KEYWORDS.	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFTN.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 183250)
TITLE	Waterston, R.H.
JOURNAL	The sequence of Homo sapiens clone
REFERENCE	unpublished
AUTHORS	2 (bases 1 to 183250)
TITLE	Waterston, R.H.
JOURNAL	Direct Submission
COMMENT	Submitted (28-OCT-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis MO 63108, USA On Mar 22, 2001 this sequence version replaced gi:12963041.

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Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
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Project Information
Center project name: H.NH0224810
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Summary Statistics
Sequencing vector: M13, 50%
Sequencing vector: Plasmid, 49%
Chemistry: Dye-Primer ET; 50% of reads
Chemistry: Dye-terminator Big Dye, 49% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181389 bases at least Q40
Consensus quality: 182006 bases at least Q30
Consensus quality: 182489 bases at least Q20
Insert size: 175000; agarose-fp
Insert size: 183150; sum-of-contigs
Quality coverage: 7.38 in Q20 bases; agarose-fp
Quality coverage: 7.26 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1187: contig of 1187 bp in length
* 1188 1287: gap of unknown length
* 1288 183250: contig of 181963 bp in length.
* Location/Qualifiers
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*     /db_xref="taxon:9606"
*     /chromosome="UNK"
*     /clone="Rp11-224B10"
*     1..1187
*       /note="assembly_name:Contig1"
*       1288..183250
*       /note="assembly_name:Contig4"
*       clone_end:SP6
*       vector_side:left"
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Best Local Similarity 43.9%; Pred. NO. 0.0029;
Matches 585; Conservative 0; Mismatches 726; Indels 23; Gaps 5;
OY 990 acacctgaacatctctctctatctataatbataatbatacagctctctagtactat 1049
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Db 16477 ACACATATTATTATTATTATATATATTAACACATATTATTATTATTATTAAT 16536
OY 1050 gtaaatgctgcacctaagatctatatatactatatatactatagctctctacac- 1108
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 16537 ACACATATTATTATTATTATATATATTTATACATATATATTTATATATATTTAAAG 16596
OY 1109 ----aaatgcatgaaactcttgcaattccaactactctgctcatctgtagctagct 1164
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Db 16597 ACATATATTATTATTATTAACATATAGTATATTTATATATATATTTAATATAGTTATA 16656
OY 1165 ttccacatgcttggaaaattagctctgagctcgaatccttaattagaacgtgttggtg 1224
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 16657 TTTCAATATATATTTATATATATGTTATATTTATTTATTTAAATATATAGTTATTTTG 16716
OY 1225 gtcaacgtttaaattcttgatattgtagcagtcacaaatcagcgctcgaacctctaca 1284
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Db 16717 ATATATATTATTATATATAGTTATTTATATATATTTATATATATAGTTATATTTAAAT 16776
OY 1285 ctaattctttaaataacacgata-----agagaaataagagtttccatgacacagt 1339

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Dp	16777	ATCTTTAATATATATAGTTATATTTAATATATATTTAATATATAGTATATATTTAATATATAT	16833
Qy	1340	tgatagtaacgtagtcgcggagatgctcaaaagcattatgagttgggttttgatggtc	1399
Dp	16637	TTAATATATATACTTTATATTTAATATATATATTTAATATATATAGTATATTTAATATATATTTT	16696
Qy	1400	agaatcgtaactagtaagacgttcctaacttttcgttagtcgttcgattagagtcgta	1459
Dp	16697	AATATATATATATTCATTTTATATATATATATTCCTTAAATATATATATTTATATATATGCTC	16556
Qy	1460	aagagctcttatttatttcaaccagctgagacttggagtcgtaglaacttgaacaacttgg	1519
Dp	16957	AATATATATATTCATATATATATTTTCCATATATATATTTTATATATATATTTTAAATATATA	17016
Qy	1520	ttgattcgaatgatttggcccatatata----aacaacactgtaattatataatgagtt	1574
Dp	17017	TATTTTATATATATATTCATATATATATATATTTTAAATATATATATTTTAAATATATTATA	17076
Qy	1575	tttttcggaatttttaacgcata-----tcgtlaagatataataacatgcagtcgttttc	1629
Dp	17077	TTAATATATATTTTAAATATATATATATTTTATATATATATTCATATATTTAATATATTTTATAT	17136
Qy	1630	aaattcatalatgaaagcagtcacgctlaagtgctactactcctacaatttgcattgagaga	1689
Dp	17137	ATATTTAATATTTAATATATATCTATATTTTAAATACATATATATTTAATTTCTATATATATATATCA	17196
Qy	1690	gatatgtaattataaatttttttcgttaagaagaataagagggaaggttaacttgggttga	1749
Dp	17197	TATATTTTATTTTATATATATATTTTAAATACATATATTCATATATTTAATATATATTTAATACA	17256
Qy	1750	tcgactgtcaaaacaaagaagaagaagcgaacccacacgaacccatcacatgatatacgacc	1809
Dp	17257	TATATTTATATTTAATATATATATATATTTAATACATATATATTTAATATATTTAATATATATAT	17316
Qy	1810	ttctatctcttttccctcttatttatttcttctcgaagacttttctcctaataigaacc	1869
Dp	17317	TTAATATATATATTTAATATATTTAATATATATTTTATATATATTTAATATATATTTAATATTTTA	17376
Qy	1870	lcccaacactcctaactaaatacaccoccatgtagaaataagaanaattatataagatttgt	1929
Dp	17377	TATATCTTTTATATTTTAAACATATATATTTTATATATATTTAATATATATTTAATATATTTT	17436
Qy	1930	tgatactttgtaactagaaaatataattgtcctcgttaatttcgtlaagttaaacaacat	1989
Dp	17437	ATATTTTATATATATATATATATATTTTAAATATATGATTTTATATTTAATATATTTTAAAA	17496
Qy	1990	ttttcagagaagaacaaatattactgcgaagaagtaggatacatatttttgcacaacaatc	2049
Dp	17497	TATATTTAATATATATTTTATATTTTATATATATTTTAAATATATTTTAAATATATTTTATAT	17556
Qy	2050	aglttagcataggggttctgtaglaaaaaacaaacacacatcttgcatttgcgcccaaaaaataa	2109
Dp	17557	TTATATATTTTAAATATATTTTAAATATATATATTTAATATATTTTAAATATATATTTTAA	17616
Qy	2110	gagagagaagaatatgttccaagaagtgtctctctctcctaattatgatttccaactaa	2169
Dp	17617	TATATATTTAATATTTTATATATTTTAAATATATATTTTAAATATATATTTTAAATATATATA	17676
Qy	2170	cccaattagatccaacagctccacaagaatccaaa--agataaacatgagacaacaattc	2226
Dp	17677	TTTTTATTTTATATATTAATATTTTATATATTTAATATATATTTTATATTTTATATATATATA	17736
Qy	2227	gatgcaaaaaaatcctcttttcaatgctcttttttatttctcctagtcctttaattactaat	2286
Dp	17737	TACATTTAATATATATTTAATATTTTATATATATTTAATATGCAATATATATATATATATAT	17796
Qy	2287	aaaaactcaacaat 2300	
Dp	17797	ATATAGTCGAATAT 17810	

RESULT 10
CNS01JRG/c

LOCUS	CNS01JRG	879 bp	DNA	SFS	17-FEB-2000
DEFINITION	Anopheles gambiae SFS T7 end of clone 14D07 of NotreDame1 library from strain PEST of Anopheles gambiae (African malaria mosquito), sequence tagged site.				
ACCESSION	AL147405				
VERSION:	ALI47405.1	GI:7005551			
KEYWORDS:	SFS.				
SOURCE	African malaria mosquito.				
ORGANISM	Anopheles gambiae				
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.				
REFERENCE	1 (bases 1 to 879)				
TITLE	Genoscope.				
JOURNAL	Direct Submission				
	Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr ; Web : www.genoscope.cns.fr)				
2 (bases 1 to 879)					
REFERENCE	Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.				
AUTHORS	Direct Submission				
TITLE	Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.				
JOURNAL	Roux, Paris 75015, France				
	This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.				
COMMENT	Location/Qualifiers				
FEATURES	1..879				
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	/strain="PEST"				
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	/clone="14D07"				
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	/note="end : T7"				
BASE COUNT	66 a 66 c 1 g 670 t 104 others				
ORIGIN					
Query Match	3.0%; Score 75; DB 53; Length 879;				
Best Local Similarity	40.7%; Pred. No. 0.0071;				
Matches 201; Conservative 51; Mismatches 241; Indels 1; Gaps 1;					
OY	433 agacaacagagaanaatcatgatgagcctatgcattcaagtccgttggttaattagaggtc 492				
Db	787 AAAAAAGGAAAGAAAAAGTAAATTAATAAAAAAATATGTGAAKAKMAAAAATTAGT 728				
OY	493 cgcctatcataaacccgtagcgcatatgcataaatcatgaaccacacacca-aaaaagtc 551				
Db	727 AAAAAARRTAGCAAADKKAKWAAAAAGKTTAAARGWMAAAAAAATAAAAAAANA 668				
OY	552 ggaactctaaatgaatgtagagaataatgaatgcccaagttggagattcaagaagagac 611				
Db	667 GKAAATRAAAAAAAAAAWAAAAAAAAAAAAAAAAAGRTTATKMKAMKMGAAAAAAKKGAA 608				
OY	612 aatgaagggtatatgacctaaacaanaatgycacatgcttggagagaggtttaat 671				
Db	607 AATTGMWGCTDAAAAAATATGAAAAAAGAGAGAKGGRGARBAAGAAGKAKAKKA 548				
OY	672 tgaacaagtgtgagattgaagaaacaagaagaagatgcacctagttcttgagata 731				
Db	547 AAAAAAATGTTAAATATGAAAAAATAKATRRRAAAAAAAMWAKAGAAAKRGWAGA 488				
OY	732 ataattacacatgctgttttatataagtaagtagagatatgacacattggttctcta 791				
Db	497 AAARRGATWKAIAAAAAAAAAATDDAAATAATRKMTTWBAAAAAGAKAKAGRTAKT 428				
OY	792 cggtgaatatgtgaagaaaaaaaaaatagtaataatttgagaaaactctanaatagtaaagg 851				
Db	427 TCDDRRAAAAAAAAAAANNNNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 368				
OY	852 tatataatgagagaagagagaagaagggggaanaatgttgcagaagatgtgaaggaggttc 911				

[illegible][illegible]


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RESULT 14
AL512783      185600 bp   DNA          HTG           19-MAR-2001
LOCUS         AL512783      Homo sapiens chromosome 10 clone RP11-462F15, *** SEQUENCING IN PROGRESS ***, 5 uncloned pieces.
ACCESSION     AL512783
VERSION       AL512783.13 GI:13396725
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     AUTHORS    Direct Submission
TITLE         Submitted (16-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
JOURNAL       On Mar 20, 2001 this sequence version replaced gi:13374823.
COMMENT       ----- Genome Center
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BA462F15
----- Summary Statistics
Assembly program: XGAP4; Version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 184826 bases at least Q40
Consensus quality: 185039 bases at least Q30
Consensus quality: 185156 bases at least Q20
Insert size: 185400; sum-of-contigs
Insert size: 175198; 7.5% error; agarose-fp
Quality coverage: 11.67x in Q20 bases; sum-of-contigs Quality coverage: 12.35x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished number as soon as it is available and the accession number will be preserved.
* 1 27247: contig of 27247 bp in length
* 27248 27347: gap of 100 bp
* 27348 29385: contig of 2038 bp in length
* 29386 29485: gap of 100 bp
* 29486 122834: contig of 93349 bp in length
* 122835 122934: gap of 100 bp
* 122935 160240: contig of 37306 bp in length
* 160241 160340: gap of 100 bp
* 160341 185600: contig of 25460 bp in length.
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/chromosome="10"
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/clone_1fb="RPC1-11.2"
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29486..122834

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159804	160341	71.4	0.018	596	6	3
1070	160341	71.4	0.018	596	6	3
159864	160341	71.4	0.018	596	6	3
1130	160341	71.4	0.018	596	6	3
159924	160341	71.4	0.018	596	6	3
1130	160341	71.4	0.018	596	6	3
159984	160341	71.4	0.018	596	6	3
1250	160341	71.4	0.018	596	6	3
160044	160341	71.4	0.018	596	6	3
1310	160341	71.4	0.018	596	6	3
160104	160341	71.4	0.018	596	6	3
1370	160341	71.4	0.018	596	6	3
160164	160341	71.4	0.018	596	6	3
1430	160341	71.4	0.018	596	6	3
160224	160341	71.4	0.018	596	6	3
1490	160341	71.4	0.018	596	6	3
160284	160341	71.4	0.018	596	6	3
1550	160341	71.4	0.018	596	6	3
160344	160341	71.4	0.018	596	6	3
1609	160341	71.4	0.018	596	6	3
160404	160341	71.4	0.018	596	6	3
1669	160341	71.4	0.018	596	6	3
160464	160341	71.4	0.018	596	6	3
1725	160341	71.4	0.018	596	6	3
160524	160341	71.4	0.018	596	6	3
1785	160341	71.4	0.018	596	6	3
160584	160341	71.4	0.018	596	6	3

Search completed: November 22, 2001, 22:16:10
Job time: 31672 sec

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	AL147405 Anopheles	/variety="Columbia"
	AC007488 Homo sapi	/db_xref="taxon:3702"
	AF203688 Canavalia	/chromosome="4"
	AC005505 Plasmodium	.2053 .3409
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	S96842 SP96-spore-	join(2053..2268,2351..2551,2625..2790,3003..3409)
	AF211124 Carsonehl	/gene="F19F18.10"
	AC010727 Homo sapi	/EC.number="1.11.1.7"
	AC011718 Homo sapi	/note="Contains Peroxidases signatures [EMBLSCAN]
	AC019041 Homo sapi	contains EST gb:H76577, Z35618, H37596, R90036, Z35219,
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	AL072596 Caenorhab	/codon.start=1
	Z92865 Caenorhabd	/product="peroxidase, prx-2"
	AL072597 Caenorhab	/protein_id="CA838291.1"
	AC009277 Homo sapi	/db_xref="GI:468977"
	AL034559 Plasmodi	/translation="MVVYKNTNLLILSLICLTLDLSSAQLRRNFYAGSCNVBOIVR
	AL355100 Homo sapi	NAOVKKVOQFTTIPATRLFLFYDCVCNCDSWIASNNNKAEKEEHLSTLAGGCG
	AX083827 Homo sapi	FDTYIRAKELDADVRCNRKYSGADITLPATPDVYNLAGGGROYDYELGRLEGLSSTA
	AX083744 Sequence	SVGGKLPHPTDVNKTLSLFARKNGSLINDMILSGAHTLGFAHCTKVFNRIYTNKTTTA
	AC087566 Mus muscu	KVPPTYNKDIYVELKASCERNIDPVALIMDPETTPROFDNYKNLOQKCLFPISDOV
	337541 Drosophila	LFTDRSKSPVDIMANNQGLEFQAFLNSMIKIGRVGVTSNGNIRRDCAFNF"
	AL355097 Homo sapi	.2053 ..2268
	AL441457 T7 end of	/gene="F19F18.10"
	AL034559 Plasmodi	/number=1
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 REFERENCE 1. (bases 42610 to 143618; 123423 to 196339)
 Rose, M., Hempel, S., Entian, K.-D., Mewes, H.-W., Lemcke, K. and
 Mayer, K.F.X.
 JOURNAL Unpublished
 REFERENCE 2. (bases 1 to 196339)
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 TITLE Direct Submission
 JOURNAL Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer